

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Bartsch, Dusan
Kandel, Eric R.
Ghirardi, Mirella

(ii) TITLE OF INVENTION: A METHOD FOR ENHANCING LONG-TERM MEMORY
IN A SUBJECT AND USES THEREOF

(iii) NUMBER OF SEQUENCES: 20

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Cooper & Dunham LLP
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(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: White, John P.
(B) REGISTRATION NUMBER: 28,678
(C) REFERENCE/DOCKET NUMBER: 50865/JPW/JML

(ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 379 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Glu Leu Asp Leu Trp Ser Glu Asp Phe Gln Leu Ala Arg Glu Trp
1 5 10 15

Gly Leu Glu Met Pro Val Val Gln Thr Asp Gly Gln Phe Gly Asp Leu
20 25 30

Lys Ser Thr Ser Arg His Gly Gly Asp Glu Ser Leu Ser Leu Gln Pro
35 40 45

Gln Gly Ala Thr Leu Lys Leu Glu Pro Phe Glu Glu Asp Val Leu Gly
50 55 60

Ala Glu Trp Met Glu Ser Ser Asp Leu Gly Ser Phe Leu Asp Ala Leu
65 70 75 80

Gly Asp Asn His Glu Arg Leu His Pro Phe Glu Ser Asn Leu Leu Glu
85 90 95

Phe Thr Ser Leu Ile Thr Pro Asp Asp Ser Thr Val Ser Lys Asp Ile
100 105 110

Leu Ser Ser Thr Leu Gln Phe Pro Thr Gln Pro Val Asn Ile Pro Leu
115 120 125

Tyr Ala Ser His Gly Ala Glu Asp Phe Ser Ala Glu Thr Glu Phe Glu
130 135 140

Asn His Leu Ser Pro Pro Asp Ser Pro Glu Gln Val Ala Pro Val Ile
145 150 155 160

Asn Leu Glu Pro Val Glu Leu Thr Ala Ser His Met Thr Val Ile Ser
165 170 175

Pro Asp Gly Leu Leu Gly Met Glu Leu Ala Ser Glu Ser Leu Thr
180 185 190

Phe Thr Glu Leu Asp Phe Val Asn Phe Asn Asp Ser Ala Val Gly Ser
195 200 205

Ile Gly Gly Ala Glu Glu Leu Leu Gly Ser Pro Leu Ser Val Asp Asp
210 215 220

Val Glu Ser Thr Ile Ser Phe Ser Gly Pro Ser Ser Pro Glu Thr Ser
225 230 235 240

Gln Ser Ser Ile Ile Glu Ser Ser Pro Glu Leu Tyr Lys Val Ile Ser
245 250 255

Thr Ser Ser Ile Asp Ala Ser Lys Arg Phe Ser Pro Tyr Ser Arg Ser
260 265 270

Ser Lys Ser Lys Gln Ser Val Lys Thr Ser Asp Ala Lys Ala Pro Arg
275 280 285

Lys Thr Arg Thr Pro Ala Gln Pro Val Pro Glu His Val Ile Met Glu
290 295 300

His Leu Asp Lys Lys Asp Arg Lys Lys Leu Gln Asn Lys Asn Ala Ala
305 310 315 320

Ile Arg Tyr Arg Met Lys Lys Gly Glu Ala Gln Gly Ile Lys Gly
325 330 335

Glu Glu Gln Glu Leu Glu Leu Asn Thr Lys Leu Lys Thr Lys Val
340 345 350

Asp Asp Leu Gln Arg Glu Ile Lys Tyr Met Lys Asn Leu Met Glu Asp
355 360 365

Val Cys Lys Ala Lys Gly Ile Gln Leu Lys Met
370 375

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Leu Asp Lys Lys Asp Arg Lys Lys Leu Gln Asn Lys Asn Ala Ala Ile
1 5 10 15

Arg Tyr Arg Met Lys Lys Gly Glu Ala Gln Gly Ile Lys Gly Glu
20 25 30

Glu Gln Glu Leu Glu Leu Asn Thr Lys Leu Lys Thr Lys Val Asp
35 40 45

Asp Leu Gln Arg Glu Ile Lys Tyr Met Lys Asn Leu Met Glu Asp Val
50 55 60

Cys Lys Ala Lys Gly Ile Gln Leu Lys
65 70

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TGACGTCA

8

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGTATTGCGT CATC

14

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACTATTGCGC AATC

14

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTCCGCTTTC CATAAGTCGA

20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ACCTGAAAAT GATATTGTAC

20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GATCCGGCGC CTCCTTGGCT GACGTCAGAG AGAGAGA

37

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GATCCGGCTG ACGTCATCAA GCTA

24

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GATCCCCTTA CGTCAGAGGC GA

22

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GATCCGGCGC GGGGCTGGCG TAGGGCCTGC GTCAGCTGCA

40

(2) INFORMATION FOR SEQ ID NO:12:

A

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GAGTGGCATC TACGTCAAGG CTTC

24

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GATCCGGCAG TATTGCGTCA TCTCAAGCTA

30

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GATCCGGCTG ACGCAATTCA AGCTA

25

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

91

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GATCCACAGT TGTGATTCA CAACCTGACC AGA

33

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GATCCGGCAC TATTGCGCAA TCTCAAGCTA

30

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GATCCATATT AAGGACATGC CG

22

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1336 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ACGCTACAGA ACGGTCAAGA AATATAATGT GTGCAAAGAT GTCTGCTTAG GAAGACACGG	60
CGACGTCCGC CCCCAAGGGC AATCGGCACA ATGGCAACCT TTCAATGATGT ATTCTAGCT	120
ACGGCTATCT CGCTTCTCTA TTGGACGGAT TTATTTATCA CATAGAAGAC TCGTATACCA	180
AACTCTACGA TGGAGCTGGA CCTTTGGAGC GAAGATTTTC AACTGGCCAG GGAATGGGGG	240
CTGGAAATGC CAGTCGTCCA GACCGATGGC CAGTTCGGTG ACCTCAAATC AACCAAGTCGT	300
CATGGTGGCG ACGAATCTCT AAGTTGCAG CCCCAGGGCG CTACACTGAA GTTGGAACCC	360
TTTGAGGAAG ATGTCCTTGG TGCAGAGTGG ATGGAGTCGT CCGATCTCGG CTCTTTCTG	420
GATGCTTGG GTGACAACCA TGAGCGGCTG CATCCGTTCG AGTCAAACTT GCTCGAGTTC	480
ACTTCTCTGA TCACTCCTGA TGATTGACCG GTGTCAAAGG ACATTCTCAG CTCAACTCTT	540
CAGTTCCAA CTCAACCAAGT GAACATCCCT TTATATGCAA GTCATGGGC CGAAGATTC	600
TCTGCAGAGA CTGAGTTGA GAACCACCTG TCGCCTCCAG ATTCTCCGGA GCAGGTAGCC	660
CCTGTCATAA ATCTAGAACCC AGTTGAACCTC ACTGCGAGCC ATATGACGGT GATCTCACCT	720
GATGGCTTGT TGGGTGGCAT GGAACCTGGCT TCAGAAAGCT TAACATTAC CGAACTAGAC	780
TTTGTGAAC TCAATGACAG TGCTGTTGGT TCAATTGGCG GTGCTGAAGA ACTTCTTGGC	840
TCCCCACTGT CAGTTGATGA TGTGGAAAGT ACAATATCAT TTTCAGGTCC ATCGTCGCCA	900
GAAACCAGCC AGAGCAGCAT CATTGAATCA AGTCCTGAAT TGTACAAAGT TATCTCTACC	960
TCGTCCATTG ATGCATCTAA GCGTTCTCT CCATACTCTC GTTCCTCCAA GTCCAAGCAA	1020
TCTGTCAAGA CTTCAGACGC TAAGGCACCT CGTAAAACGA GGACACCGGC GCAGCCTGTG	1080
CCAGAACATG TCATCATGGA ACATTTGGAC AAAAAGGACA GAAAGAAGCT TCAGAACAAAG	1140
AATGCTGCCA TTAGGTATAG GATGAAGAAG AAGGGGGAGG CTCAGGGCAT CAAAGGGGAG	1200
GAACAGGAAT TAGAAGAACT CAACACAAAG CTTAAGACTA AGGTCGATGA CTTGCAAAGA	1260

GAAATCAAGT ACATGAAAAA TTTAATGGAA GATGTTGCA AGGCGAAAGG TATTCAGCTT 1320
AAATAGTGGG AAGGGT 1336

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Leu Asp Lys Lys Leu Lys Lys Met Glu Gln Asn Lys Thr Ala Ala Thr
1 5 10 15

Arg Tyr Arg Gln Lys Lys Arg Ala Glu Gln Glu Ala Leu Thr Gly Glu
20 25 30

Cys Lys Glu Leu Glu Lys Lys Asn Glu Ala Leu Lys Glu Lys Ala Asp
35 40 45

Ser Leu Ala Lys Glu Ile Gln Tyr Leu Lys Asp Leu Ile Glu Glu Val
50 55 60

Arg Lys Ala Arg Gly Lys Lys Arg Val Pro
65 70

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Leu Asp Lys Lys Leu Lys Lys Met Glu Gln Asn Lys Thr Ala Ala Thr
1 5 10 15

Arg Tyr Arg Gln Lys Lys Arg Ala Glu Gln Glu Ala Leu Thr Gly Glu
20 25 30

Cys Lys Glu Leu Glu Lys Lys Asn Glu Ala Leu Lys Glu Arg Ala Asp
35 40 45

Ser Leu Ala Lys Glu Ile Gln Tyr Leu Lys Asp Leu Ile Glu Glu Val
50 55 60

Arg Lys Ala Arg Gly Lys Lys Arg Val Pro
65 70
